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STRUCTURAL ANALYSIS AND MODELING COMPARISON OF PRIMATES' AMYLOID βA4 PROTEIN

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A dissertation submitted in partial fulfillment of the
requirements for the award of the degree of
Master of Science (Biotechnology)

Faculty of Bioscience and Bioengineering
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January 2013

To my beloved family and fiancé

ACKNOWLEDGMENT

I would like to begin by sincerely thanking my supervisor, Associated Prof Dr. Shahir Shamsir for his constant support, guidance and mentorship over the course of this thesis. He gave me the freedom to define my thesis statements. I am very grateful to having the opportunity for work on this thesis.

I am heartily thankful to my parents, for their unconditional supports and encouraging me to continue my education. I am very grateful to my lovely fiance for his professional gaudiness and emotional supports.

ABSTRACT

Amyloid protein originally termed "beta-protein" or "amyloid A4" which is indicated as "beta A4." Amyloid beta A4 protein is proteolytically derived from a transmembrane protein named amyloid precursor protein (APP) which is encoded by an extensively expressed gene on chromosome 21. Mutations in Amyloid βA4 gene cause the plaques which are composed of a tangle of regularly ordered fibrillar aggregates called amyloid fibers, and abnormal accumulation of amyloid fibrils make protein misfolding diseases so that it leads to amyloidosis and neurodegenerative disorder like Alzheimer diseases (AD) or Parkinson diseases (PD).Currently there are 91 structure of Amyloid beta A4 protein have been predicted in various species, but there is no presently concrete evidence that shows Amyloid beta A4 model in primates. This study was focus on Amyloid beta A4 protein information and analyzed using bioinformatics software such as: Uniprot, Deep View, PDB (protein data bank), Swiss Model, Jal View, BLAST, VMD(Visual molecular dynamics), NCBI(National center for biotechnology information) therefore those of programs help us to predict and create a new model of 3D structure for this protein and they are useful for analysis multiple alignment, simulation , image processing for βA4 protein sequence, illustrate conserved regions and residues of protein between different species (human being and primates) to indicate comparison of their structural features and their gen properties to this end 8 primates were chosen. Based on the analysis of this comparison demonstrated that some of the primates are highly conserved with their template (Homo sapiens) and they have similar primary and tertiary structure with template .The reason of this issue is that in all of them the protein's gene location is on chromosome 21 as same as human gen location. On the other hand rest of chosen primates is not conserved with template and their structures are totally different with Homo sapiens due to APP gene location is on chromosome 3 instead of chromosome 21. This information was gathered from GenBank which is the genetic sequence database, an annotated collection of all publicly available DNA sequences.

ABSTRAK

Amiloid protein asalnya dipanggil "beta-protein" atau "A4 amyloid" yang ditandakan sebagai "A4 beta." Beta amiloid protein A4 proteolytically diperolehi daripada protein transmembran pelopor protein amiloid dinamakan (APP) yang dikodkan oleh gene meluas dinyatakan pada 21 kromosom. Mutasi dalam gen βA4 amiloid menyebabkan plak yang terdiri daripada kekusutan agregat kerap diperintahkan berhubung dgn urat saraf dipanggil serat amiloid, dan pengumpulan abnormal gentian halus amiloid membuat penyakit misfolding protein supaya ia membawa kepada amyloidosis dan gangguan neurodegenerative seperti penyakit Alzheimer (AD) atau Parkinson penyakit (PD). Pada masa ini terdapat 91 struktur protein amiloid beta A4 telah diramalkan dalam pelbagai spesis, tetapi tidak ada bukti yang kini konkrit yang menunjukkan amiloid beta A4 model dalam primat. Kajian ini adalah memberi tumpuan kepada protein amiloid beta maklumat A4 dan dianalisis menggunakan perisian bioinformatik seperti: Uniprot, Deep View, PDB (protein data bank), Model Switzerland, Jal View, letupan, VMD (Visual molekul dinamik), NCBI (National pusat maklumat bioteknologi) itu mereka program membantu kita untuk meramalkan dan mewujudkan satu model baru struktur 3D protein ini dan mereka adalah berguna untuk penjajaran pelbagai analisis, simulasi, pemprosesan imej untuk βA4 urutan protein, menggambarkan kawasan terpelihara dan sisa protein antara spesies yang berbeza (manusia dan primat) untuk menunjukkan perbandingan ciri-ciri struktur mereka dan sifat-sifat gen mereka untuk tujuan ini 8 primat telah dipilih. Berdasarkan analisis perbandingan ini menunjukkan bahawa beberapa primat sangat dipelihara dengan template (Homo sapiens) mereka dan mereka mempunyai struktur yang serupa utama dan tertiari dengan template. Sebab isu ini adalah bahawa dalam semua daripada mereka lokasi gen-protein ini adalah pada 21 kromosom yang sama sebagai lokasi gen manusia. Pada rehat tangan lain primat yang dipilih tidak dipelihara dengan template dan struktur mereka adalah sama sekali berbeza dengan Homo sapiens disebabkan lokasi gen APP adalah pada 3 kromosom bukannya kromosom 21. Maklumat ini dikumpulkan dari GenBank yang merupakan pangkalan data jujukan genetik, koleksi beranotasi semua jujukan DNA yang boleh didapati oleh orang ramai.